RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002
TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
  4 <110> APPLICANT: Dranoff, Glenn
  5         Schmollinger, Jan
  6         Hodi, F. Stephen
  7         Mollick, Joseph
  9 <120> TITLE OF INVENTION: TUMOR ANTIGENS AND USES THEREOF
 12 <130> FILE REFERENCE: 2486/109 (formerly 50059/005002)
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/762,577A
C--> 14 <141> CURRENT FILING DATE: 2002-08-29
 14 <150> PRIOR APPLICATION NUMBER: 60/095,766
 15 <151> PRIOR FILING DATE: 1998-08-07
 17 <160> NUMBER OF SEQ ID NOS: 68
 19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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495 <210> SEQ ID NO: 10
496 <211> LENGTH: 1168
497 <212> TYPE: PRT
498 <213> ORGANISM: Homo sapiens
500 <400> SEQUENCE: 10
501 Asn Ile Asp Leu Asp Leu Glu Ile Val Gln Ser Leu Gln His Gly His
502 1               5                   10                  15
503 Gly Gly Trp Thr Asp Gly Met Phe Glu Thr Leu Thr Thr Thr Gly Thr
504             20                  25                  30
505 Val Cys Gly Ile Asp Glu Asp His Asp Ile Val Val Gln Tyr Pro Ser
506         35                  40                  45
507 Gly Asn Arg Trp Thr Phe Asn Pro Ala Val Leu Thr Lys Ala Asn Ile
508         50                  55                  60
509 Val Arg Ser Gly Asp Ala Ala Gln Gly Ala Glu Gly Gly Thr Ser Gln
510 65                  70                  75                  80
511 Phe Gln Val Gly Asp Leu Val Gln Val Cys Tyr Asp Leu Glu Arg Ile
512                 85                  90                  95
513 Lys Leu Leu Gln Arg Gly His Gly Glu Trp Ala Glu Ala Met Leu Pro
514                 100                 105                 110
515 Thr Leu Gly Lys Val Gly Arg Val Gln Gln Ile Tyr Ser Asp Ser Asp
516             115                 120                 125
517 Leu Lys Val Glu Val Cys Gly Thr Ser Trp Thr Tyr Asn Pro Ala Ala
518         130                 135                 140
519 Val Ser Lys Val Ala Ser Ala Gly Ser Ala Ile Ser Asn Ala Ser Gly
520 145                 150                 155                 160
521 Glu Arg Leu Ser Gln Leu Leu Lys Lys Leu Phe Glu Thr Gln Glu Ser
522                 165                 170                 175
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621  Leu Phe Ser Arg Phe Lys Arg Asn Ile Val Glx Leu Glu Ser Asp Tyr
                         965                 970                 975
622  Gln Phe Gln Gly Asp Glx Glx Thr Arg Lys Gly Lys Ile Ser Asn Asn
623                  980                 985                 990
624  Ser Gly Gln Leu Lys Arg Lys Lys Lys Arg Val Ser Ile Asn Trp Pro
625                  995                 1000                1005
626  Leu Thr Val Ala Phe Leu Thr Leu Ile Tyr Thr Leu Phe Cys Ser Ala
627             1010                1015                1020
628  Ser Val Phe Lys Lys Asn Leu Glx Lys Val Tyr Phe Arg Phe Ser Val
629             1025                1030                1035                    ←1040
E--> 630  Ile Thr Tyr Leu Gly Leu Ile Glx Pro Val Lys Glx His Cys Pro Ile
631             1045                1050                1055
632  Trp Thr Ser Glu Val Leu Phe Ser Phe Ala Asp Val His Ser Ile Pro
633             1060                1065                1070
634  Val Ile Cys Lys Ile Asn Ala Phe Ser Lys Lys Lys Ser Phe Leu Leu
635             1075                1080                1085
636  Cys Ile Ser Glx Phe Glx Gln Cys Glx Glx Phe Cys Leu His Tyr Arg
637             1090                1095                1100
638  Pro Tyr Phe His Tyr Leu Phe Leu Tyr Ser Ile Phe Cys Tyr Lys Glu
639             1105                1110                1115                    ←1120
E--> 640  Asn Ser Leu Ser Val Tyr Thr Tyr Gly Glx Gly Tyr Tyr Leu Asn Cys
641             1125                1130                1135
642  Gln Gln Tyr Pro Arg His Gly Gln Glx Pro Asn Tyr Lys Tyr Phe Arg
643             1140                1145                1150
644  Lys Ser Asp Gln Asp Met Tyr Arg Asn Val Cys Leu Pro Val Asp Phe
645             1155                1160                1165
646
1510 <210> SEQ ID NO: 40
1511 <211> LENGTH: 309
1512 <212> TYPE: DNA
1513 <213> ORGANISM: Homo sapiens
1515 <400> SEQUENCE: 40
E--> 1516  ncaaagtcaa atgaatttat tcagaaaagg ccttgcttgg tatcagacta agaaaagcag   60
E--> 1517  ccctgcccgc cgcccccan tccagaaggg tcaatttaca aagacagggg cgcagggag   120
1518  agctgggtgg ggaagacaca gccaggccag gagcttctgc aggccttggg cttccctgag   180
1519  ggcctcgcgg cttctgggtg gctgctatag tggccccaca ggaggccatg cactgtgggg   240
E--> 1520  gtcattgggt cacngggtca cgaangcata gcctnagggg gnagcccgtn agcagctccg   300
E--> 1521  gganggccc                                                          309
1533 <210> SEQ ID NO: 42
1534 <211> LENGTH: 166
1535 <212> TYPE: DNA
1536 <213> ORGANISM: Homo sapiens
1538 <400> SEQUENCE: 42
E--> 1539  cggcctgcag aagcntcctg gncntggttg ttttttcccc acccagctct cccctgcgcc   60
E--> 1540  cctttttttt taaatnnacc cttctggagt gggggcggc gggcagggct gctttttna   120
E--> 1541  gtctgatgcc aagcaaggcc tttttgaat aanttcattt ganttt                   166
1543 <210> SEQ ID NO: 43
1544 <211> LENGTH: 209
1545 <212> TYPE: DNA
1546 <213> ORGANISM: Homo sapiens
```

move over to the left, one space, and add the "∅".

Ns deleted, see p.11 for explanation

some error

```
   1548  <400> SEQUENCE: 43                                                           60
E--> 1549  gaaggtggat naggGtgctg tggacagtgc tacggtggcc agtggtggtg cccagacctt           120
E--> 1550  ggcccttgcc gggtcccctg ccccatcgcn cggccaaggc tggacacagt gagaacgggg           180
E--> 1551  ttgaggagga cacagaangt caaacggggc ccaaagaagg tacccntggg gagcccatca           209
E--> 1552  gagancccan gccccagccn ggcagggac
     1674  <210> SEQ ID NO: 46
     1675  <211> LENGTH: 1299
     1676  <212> TYPE: PRT
     1677  <213> ORGANISM: Homo sapiens
     1679  <400> SEQUENCE: 46
     1680  Met Glu Pro Pro Ser Cys Ile Gln Asp Glu Pro Phe Pro His Pro Leu
     1681   1               5                  10                  15
     1682  Glu Pro Glu Pro Gly Val Ser Ala Gln Pro Gly Pro Gly Lys Pro Ser
     1683          20                  25                  30
     1684  Asp Lys Arg Phe Arg Leu Trp Tyr Val Gly Gly Ser Cys Leu Asp His
     1685          35                  40                  45
     1686  Arg Thr Thr Leu Pro Met Leu Pro Trp Leu Met Ala Glu Ile Arg Arg
     1687       50                  55                  60
     1688  Arg Ser Gln Lys Pro Glu Ala Gly Gly Cys Gly Ala Pro Ala Ala Arg
     1689   65                  70                  75                  80
     1690  Glu Val Ile Leu Val Leu Ser Ala Pro Phe Leu Arg Cys Val Pro Ala
     1691                  85                  90                  95
     1692  Pro Gly Ala Gly Ala Ser Gly Gly Thr Ser Pro Ser Ala Thr Gln Pro
     1693              100                 105                 110
     1694  Asn Pro Ala Val Phe Ile Phe Glu His Lys Ala Gln His Ile Ser Arg
     1695          115                 120                 125
     1696  Phe Ile His Asn Ser His Asp Leu Thr Tyr Phe Ala Tyr Leu Ile Lys
     1697          130                 135                 140
     1698  Ala Gln Pro Asp Asp Pro Glu Ser Gln Met Ala Cys His Val Phe Arg
     1699  145                 150                 155                 160
     1700  Ala Thr Asp Pro Ser Gln Val Pro Asp Val Ile Ser Ser Ile Arg Gln
     1701                  165                 170                 175
     1702  Leu Ser Lys Ala Ala Met Lys Glu Asp Ala Lys Pro Ser Lys Asp Asn
     1703              180                 185                 190
     1704  Glu Asp Ala Phe Tyr Asn Ser Gln Lys Phe Glu Val Leu Tyr Cys Gly
     1705          195                 200                 205
     1706  Lys Val Thr Val Thr His Lys Lys Ala Pro Ser Ser Leu Ile Asp Asp
     1707          210                 215                 220
     1708  Cys Met Glu Lys Phe Ser Leu His Glu Gln Gln Arg Leu Lys Ile Gln
     1709  225                 230                 235                 240
     1710  Gly Glu Gln Arg Gly Pro Asp Pro Gly Glu Asp Leu Ala Asp Leu Glu
     1711                  245                 250                 255
     1712  Val Val Val Pro Gly Ser Pro Gly Asp Cys Leu Pro Glu Glu Ala Asp
     1713              260                 265                 270
     1714  Gly Thr Asp Thr His Leu Gly Leu Pro Ala Gly Ala Ser Gln Pro Ala
     1715          275                 280                 285
     1716  Leu Thr Ser Ser Arg Val Cys Phe Pro Glu Arg Ile Leu Glu Asp Ser
     1717          290                 295                 300
     1718  Gly Phe Asp Glu Gln Gln Glu Phe Arg Ser Arg Cys Ser Ser Val Thr
```

```
1768  Ala Pro Ser Phe Thr Ala Pro Ser Phe Leu Lys Ser Phe Tyr Gln Asn
1769  705             710             715                     720
1770  Ser Gly Arg Leu Ser Pro Gln Tyr Glu Asn Glu Ile Arg Gln Asp Thr
1771              725             730                     735
1772  Ala Ser Glu Ser Ser Asp Gly Glu Gly Arg Lys Arg Thr Ser Ser Thr
1773              740             745             750
1774  Cys Ser Asn Glu Ser Leu Ser Val Gly Gly Thr Ser Val Thr Pro Arg
1775          755             760             765
1776  Arg Ile Ser Trp Arg Gln Arg Ile Phe Leu Arg Val Ala Ser Pro Met
1777      770             775             780
1778  Asn Lys Ser Pro Ser Ala Met Gln Gln Gln Asp Gly Leu Asp Arg Asn
1779  785             790             795                     800
1780  Glu Leu Leu Pro Leu Ser Pro Leu Ser Pro Thr Met Glu Glu Glu Pro
1781              805             810             815
1782  Leu Val Ile Phe Leu Ser Gly Glu Asp Asp Pro Glu Lys Ile Glu Glu
1783              820             825             830
1784  Arg Lys Lys Ser Lys Glu Leu Arg Ser Leu Trp Arg Lys Ala Ile His
1785          835             840             845
1786  Gln Gln Ile Leu Leu Leu Arg Met Glu Lys Glu Asn Gln Lys Leu Glu
1787      850             855             860
1788  Gly Ala Ser Arg Asp Glu Leu Gln Ser Arg Lys Val Lys Leu Asp Tyr
1789  865             870             875                     880
1790  Glu Glu Val Gly Ala Cys Gln Lys Glu Val Leu Ile Thr Trp Asp Lys
1791              885             890             895
1792  Lys Leu Leu Asn Cys Arg Ala Lys Ile Arg Cys Asp Met Glu Asp Ile
1793              900             905             910
1794  His Thr Leu Leu Lys Glu Gly Val Pro Lys Ser Arg Arg Gly Glu Ile
1795          915             920             925
1796  Trp Gln Phe Leu Ala Leu Gln Tyr Arg Leu Arg His Arg Leu Pro Asn
1797      930             935             940
1798  Lys Gln Gln Pro Pro Asp Ile Ser Tyr Lys Glu Leu Leu Lys Gln Leu
1799  945             950             955                     960
1800  Thr Ala Gln Gln His Ala Ile Leu Val Asp Leu Gly Arg Thr Phe Pro
1801              965             970                     975
1802  Thr His Pro Tyr Phe Ser Val Gln Leu Gly Pro Gly Gln Leu Ser Leu
1803              980             985             990
1804  Phe Asn Leu Leu Lys Ala Tyr Ser Leu Leu Asp Lys Glu Val Gly Tyr
1805          995             1000            1005
1806  Cys Gln Gly Ile Ser Phe Val Ala Gly Val Leu Leu His Met Ser
1807      1010            1015            1020
1808  Glu Glu Gln Ala Phe Glu Met Leu Lys Phe Leu Met Tyr Asp Leu Gly
1809  1025            1030            1035                    1040
1810  Phe Arg Lys Gln Tyr Arg Pro Asp Met Met Ser Leu Gln Ile Gln Met
1811              1045            1050            1055
1812  Tyr Gln Leu Ser Arg Leu Leu His Asp Tyr His Arg Asp Leu Tyr Asn
1813              1060            1065            1070
1814  His Leu Glu Glu Asn Glu Ile Ser Pro Ser Leu Tyr Ala Ala Pro Trp
1815          1075            1080            1085
1816  Phe Leu Thr Leu Phe Ala Ser Gln Phe Ser Leu Gly Phe Val Ala Arg
```

E--> 1809   (with arrow markers near 1025, 1030, 1035, ←1040)

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Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
      1817     1090             1095              1100
      1818  Val Phe Asp Ile Ile Phe Leu Gln Gly Thr Glu Val Ile Phe Lys Val
E--> 1819  1105             1110              1115             ←1120
      1820  Ala Leu Ser Leu Leu Ser Ser Gln Glu Thr Leu Ile Met Glu Cys Glu
      1821                   1125              1130             1135
      1822  Ser Phe Glu Asn Ile Val Glu Phe Leu Lys Asn Thr Leu Pro Asp Met
      1823             1140        .        1145             1150
      1824  Asn Thr Ser Glu Met Glu Lys Ile Ile Thr Gln Val Phe Glu Met Asp
      1825        . 1155        .        1160             1165
      1826  Ile Ser Lys Gln Leu His Ala Tyr Glu Val Glu Tyr His Val Leu Gln
      1827        1170             1175             1180
      1828  Asp Glu Leu Gln Glu Ser Ser Tyr Ser Cys Glu Asp Ser Glu Thr Leu
E--> 1829  1185             1190              1195             ←1200
      1830  Glu Lys Leu Glu Arg Ala Asn Ser Gln Leu Lys Arg Gln Asn Met Asp
      1831   ,                1205              1210             1215
      1832  Leu Leu Glu Lys Leu Gln Val Ala His Thr Lys Ile Gln Ala Leu Glu
      1833             1220             1225             1230
      1834  Ser Asn Leu Glu Asn Leu Leu Thr Arg Glu Thr Lys Met Lys Ser Leu
      1835        1235             1240             1245
      1836  Ile Arg Thr Leu Glu Gln Glu Lys Met Ala Tyr Gln Lys Thr Val Glu
      1837        1250             1255             1260
      1838  Gln Leu Arg Lys Leu Leu Pro Ala Asp Ala Leu Ala Asn Cys Asp Leu
E--> 1839  1265             1270              1275             ←1280
      1840  Leu Leu Arg Asp Leu Asn Cys Asn Pro Asn Asn Lys Ala Lys Ile Gly
      1841                   1285        .        1290             1295
      1842  Asn Lys Pro
      1969  <210> SEQ ID NO: 49
      1970  <211> LENGTH: 226
      1971  <212> TYPE: DNA
      1972  <213> ORGANISM: Homo sapiens
      1974  <400> SEQUENCE: 49
      1975  ctgggatact cccctcccag ggtgtctggt ggcaggcctg tgcctatccc tgctgtcccc     60
      1976  agggtgggcc ccggggggtca ggagctccag aagggccagc tgggcatatt ctgagattgg    120
E--> 1977  ccatcagccc ccatttctgc tgcaaacctg gtcagagcca gtnttccntc catgggacct    180
      1978  aaagacagtg ccaagtgcct gcaccgtgga ccacagccga gccact               226
      2262  <210> SEQ ID NO: 62
      2263  <211> LENGTH: 607
      2264  <212> TYPE: DNA
      2265  <213> ORGANISM: Homo sapiens
      2267  <400> SEQUENCE: 62
      2268  ttttcagcat gagaatatgt gaatatgttt atttaggttt aacttacttc ttactatata     60
      2269  gatttggctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag    120
      2270  taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag    180
      2271  aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg    240
      2272  atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc    300
      2273  agatgaagat gtgccttcct ctgagtggtg aaatccagat gtagtcagtg gttttctttc    360
      2274  ttccattact gctgcagcag aactgagagc ccaatctttt attagatctt tatgttttc    420
      2275  gttgataaca ggcctattat aatccgattg tcatctactc caaacacaac agctggtctg    480 ·
      2276  atgctttcag tagccggacc tctgtagctt ttgtgttcga atggtggcgt ctaagtgttc    540
```

No found -see p11

```
      2277  ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg    600
                                                                                607
E--> 2278  tncatca
      2280  <210> SEQ ID NO: 63
      2281  <211> LENGTH: 402
      2282  <212> TYPE: DNA
      2283  <213> ORGANISM: Homo sapiens
      2285  <400> SEQUENCE: 63
E--> 2286  ggcagagcac agaccaagcc aggagatgga taaaggttaa aaaatcaagc aacttctgct    60
      2287  acttctgaaa aggataatga tgatgaccaa agtgacaagg gtacttatac cattgagtta    120
      2288  gagaatccca acagtgagga agtggaagca agaaaaatga ttcacaaggt aaataattga    180
      2289  aatttgagtg tgatcttagt tgttgtgtgg tgtatttgac tggtggaaat tattggagag    240
      2290  tcagcatgag atgttgtcat gcagtcagtg gtatgtgaat tttagggttt tattagggaa    300
      2291  ctgcaagact aacagtaaga ccaacatgct ttgtgatttt atttgctgat attctgaatt    360
      2292  tacctgagtt tcatacataa agctctgtac atttaaaagg tt                       402
      2294  <210> SEQ ID NO: 64
      2295  <211> LENGTH: 607
      2296  <212> TYPE: DNA
      2297  <213> ORGANISM: Homo sapiens
      2299  <400> SEQUENCE: 64
      2300  ttttcagcat gagaatatgt gaatatgttt atttaggttt aacttacttc ttactatata    60
      2301  gatttggctt gttttttata ataacaactg atatatgatt cacaaaaaag cagagaagag    120
      2302  taagagaaag agagagaaat ggagaaagag aagaaaaaag ggataaagaa tgaaagagag    180
      2303  aaagagaata ccattctcta aaggaagagg tgcagaaaat tccattatcc tttcttcttg    240
      2304  atcatgcctt gtatgattgg cagccaaact agcccactgt gaaacccaac gtttgcttcc    300
      2305  agatgaagat gtgccttcct ctgagtggtg aaatccagat gtagtcagtg gtttctcttc    360
      2306  ttccattact gctgcagcag aactgagagc ccaatctttt attagatctt tatgttttc    420
      2307  gttgataaca ggcctattat aatccgattg tcatctactc caaacacaac agctggtctg    480
      2308  atgctttcag tagccggacc tctgtagctt ttgtgttcga atggtggcgt ctaagtgttc    540
      2309  ctcaagagtt gcacgtttgc tacagcgccg tgagccccag cgttctctga atcacttgcg    600
                                                                                607
 E--> 2310  tncatca
      2312  <210> SEQ ID NO: 65
      2313  <211> LENGTH: 317
      2314  <212> TYPE: DNA
      2315  <213> ORGANISM: Homo sapiens
      2317  <400> SEQUENCE: 65
E--> 2318  tggggcgtgt gtggaanaac gttantgccc agcggantag nggccccgga gcncgaccgc    60
E--> 2319  agcggcanan cgacaacagc ggcgacgacg acgacgacga ggtgggggga ggacggcgtg    120
E--> 2320  cgagagactc acgggacgcg acgncccgc ctcccccgtc cggtccctct ctccacggta    180
      2321  aggggatgac gtagctttgc caaagactta gaagctaagc agaaaatgag cttaacatcc    240
      2322  tggttttgg tgagcagtgg aggcactcgc cacaggctgc cacgagaaat gatttttgtt    300
      2323  ggaaaaaatg actgtga                                                    317
      2473  <210> SEQ ID NO: 68
      2474  <211> LENGTH: 2349
      2475  <212> TYPE: PRT
      2476  <213> ORGANISM: Homo sapiens
      2478  <400> SEQUENCE: 68
      2479  Met Ala Ala Val Leu Gln Gln Val Leu Glu Arg Thr Glu Leu Asn Lys
      2480   1               5                  10                  15
      2481  Leu Pro Lys Ser Val Gln Asn Lys Leu Glu Lys Phe Leu Ala Asp Gln
```

```
                             805                    810                    815
2580
2581     Thr Asn Leu Gln Thr Ile Gln Gly Ile Leu Glu Arg Ser Glu Thr Glu
2582               820                    825                    830
2583     Thr Lys Gln Arg Leu Ser Ser Gln Ile Glu Lys Leu Glu His Glu Ile
2584               835                    840                    845
2585     Ser His Leu Lys Lys Lys Leu Glu Asn Glu Val Glu Gln Arg His Thr
2586               850                    855                    860
2587     Leu Thr Arg Asn Leu Asp Val Gln Leu Leu Asp Thr Lys Arg Gln Leu
2588     865                    870                    875                    880
2589     Asp Thr Glu Thr Asn Leu His Leu Asn Thr Lys Glu Leu Leu Lys Asn
2590                   885                    890                    895
2591     Ala Gln Lys Glu Ile Ala Thr Leu Lys Gln His Leu Ser Asn Met Glu
2592                   900                    905                    910
2593     Val Gln Val Ala Ser Gln Ser Ser Gln Arg Thr Gly Lys Gly Gln Pro
2594               915                    920                    925
2595     Ser Asn Lys Glu Asp Val Asp Asp Leu Val Ser Gln Leu Arg Gln Thr
2596     930                    935                    940
2597     Glu Glu Gln Val Asn Asp Leu Lys Glu Arg Leu Lys Thr Ser Thr Ser
2598     945                    950                    955                    960
2599     Asn Val Glu Gln Tyr Gln Ala Met Val Thr Ser Leu Glu Glu Ser Leu
2600                   965                    970                    975
2601     Asn Lys Glu Lys Gln Val Thr Glu Glu Val Arg Lys Asn Ile Glu Val
2602               980                    985                    990
2603     Arg Leu Lys Glu Ser Ala Glu Phe Gln Thr Gln Leu Glu Lys Lys Leu
2604               995                    1000                   1005
2605     Met Glu Val Glu Lys Glu Lys Gln Glu Leu Gln Asp Asp Lys Arg Arg
2606         1010                   1015                   1020
2607     Ala Ile Glu Ser Met Glu Gln Gln Leu Ser Glu Leu Lys Lys Thr Leu
E--> 2608     1025                   1030                   1035               ←1040
2609     Ser Ser Val Gln Asn Glu Val Gln Glu Ala Leu Gln Arg Ala Ser Thr
2610               1045                   1050                   1055
2611     Ala Leu Ser Asn Glu Gln Gln Ala Arg Arg Asp Cys Gln Glu Gln Ala
2612               1060                   1065                   1070
2613     Lys Ile Ala Val Glu Ala Gln Asn Lys Tyr Glu Arg Glu Leu Met Leu
2614               1075                   1080                   1085
2615     His Ala Ala Asp Val Glu Ala Leu Gln Ala Ala Lys Glu Gln Val Ser
2616         1090                   1095                   1100
2617     Lys Met Ala Ser Val Arg Gln His Leu Glu Glu Thr Thr Gln Lys Ala
E--> 2618     1105                   1110                   1115               ←1120
2619     Glu Ser Gln Leu Leu Glu Cys Lys Ala Ser Trp Glu Glu Arg Glu Arg
2620               1125                   1130                   1135
2621     Met Leu Lys Asp Glu Val Ser Lys Cys Val Cys Arg Cys Glu Asp Leu
2622               1140                   1145                   1150
2623     Glu Lys Gln Asn Arg Leu Leu His Asp Gln Ile Glu Lys Leu Ser Asp
2624         1155                   1160                   1165
2625     Lys Val Val Ala Ser Val Lys Glu Gly Val Gln Gly Pro Leu Asn Val
2626         1170                   1175                   1180
2627     Ser Leu Ser Glu Glu Gly Lys Ser Gln Glu Gln Ile Leu Glu Ile Leu
E--> 2628     1185                   1190                   1195               ←1200
```

```
      2629  Arg Phe Ile Arg Arg Glu Lys Glu Ile Ala Glu Thr Arg Phe Glu Val
                        1205                1210                1215
      2630  Ala Gln Val Glu Ser Leu Arg Tyr Arg Gln Arg Val Glu Leu Leu Glu
                        1220                1225                1230
      2631
      2632  Arg Glu Leu Gln Glu Leu Glu Asp Ser Leu Asn Ala Glu Arg Glu Lys
                        1235                1240                1245
      2633
      2634  Val Gln Val Thr Ala Lys Thr Met Ala Gln His Glu Glu Leu Met Lys
      2635           1250                1255                1260
      2636  Lys Thr Glu Thr Met Asn Val Val Met Glu Thr Asn Lys Met Leu Arg
      2637           1265                1270                1275             1280
E--> 2638  Glu Glu Lys Glu Arg Leu Glu Gln Asp Leu Gln Gln Met Gln Ala Lys
      2639                1285                1290                1295
      2640  Val Arg Lys Leu Glu Leu Asp Ile Leu Pro Leu Gln Glu Ala Asn Ala
      2641                1300                1305                1310
      2642  Glu Leu Ser Glu Lys Ser Gly Met Leu Gln Ala Glu Lys Lys Leu Leu
      2643           1315                1320                1325
      2644  Glu Glu Asp Val Lys Arg Trp Lys Ala Arg Asn Gln His Leu Val Ser
      2645           1330                1335                1340
      2646  Gln Gln Lys Asp Pro Asp Thr Glu Glu Tyr Arg Lys Leu Leu Ser Glu
      2647           1345                1350                1355             1360
E--> 2648  Lys Glu Val His Thr Lys Arg Ile Gln Gln Leu Thr Glu Glu Ile Gly
      2649                1365                1370                1375
      2650  Arg Leu Lys Ala Glu Ile Ala Arg Ser Asn Ala Ser Leu Thr Asn Asn
      2651                1380                1385                1390
      2652  Gln Asn Leu Ile Gln Ser Leu Lys Glu Asp Leu Asn Lys Val Arg Thr
      2653           1395                1400                1405
      2654  Glu Lys Glu Thr Ile Gln Lys Asp Leu Asp Ala Lys Ile Ile Asp Ile
      2655           1410                1415                1420
      2656  Gln Glu Lys Val Lys Thr Ile Thr Gln Val Lys Lys Ile Gly Arg Arg
      2657           1425                1430                1435             1440
E--> 2658  Tyr Lys Thr Gln Tyr Glu Glu Leu Lys Ala Gln Gln Asp Lys Val Met
      2659                1445                1450                1455
      2660  Glu Thr Ser Ala Gln Ser Ser Gly Asp His Gln Glu Gln His Val Ser
      2661                1460                1465                1470
      2662  Val Gln Glu Met Gln Glu Leu Lys Glu Thr Leu Asn Gln Ala Glu Thr
      2663           1475                1480                1485
      2664  Lys Ser Lys Ser Leu Glu Ser Gln Val Glu Asn Leu Gln Lys Thr Leu
      2665           1490                1495                1500
      2666  Ser Glu Lys Glu Thr Glu Ala Arg Asn Leu Gln Glu Gln Thr Val Gln
      2667           1505                1510                1515             1520
E--> 2668  Leu Gln Ser Glu Leu Ser Arg Leu Arg Gln Asp Leu Gln Asp Arg Thr
      2669                1525                1530                1535
      2670  Thr Gln Glu Glu Gln Leu Arg Gln Gln Ile Thr Glu Lys Glu Glu Lys
      2671                1540                1545                1550
      2672  Thr Arg Lys Ala Ile Val Ala Ala Lys Ser Lys Ile Ala His Leu Ala
      2673           1555                1560                1565
      2674  Gly Val Lys Asp Gln Leu Thr Lys Glu Asn Glu Glu Leu Lys Gln Arg
      2675           1570                1575                1580
      2676
      2677  Asn Gly Ala Leu Asp Gln Gln Lys Asp Glu Leu Asp Val Arg Ile Thr
```

RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: US/09/762,577A   TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
E--> 2678 1585           1590           1595            ⊲1600
     2679 Ala Leu Lys Ser Gln Tyr Glu Gly Arg Ile Ser Arg Leu Glu Arg Glu
     2680           1605           1610           1615
     2681 Leu Arg Glu His Gln Glu Arg His Leu Glu Gln Arg Asp Glu Pro Gln
     2682           1620           1625           1630
     2683 Glu Pro Ser Asn Lys Val Pro Glu Gln Gln Arg Gln Ile Thr Leu Lys
     2684      1635           1640           1645
     2685 Thr Thr Pro Ala Ser Gly Glu Arg Gly Ile Ala Ser Thr Ser Asp Pro
     2686      1650           1655           1660
     2687 Pro Thr Ala Asn Ile Lys Pro Thr Pro Val Val Ser Thr Pro Ser Lys
E--> 2688 1665           1670           1675            ⊲1680
     2689 Val Thr Ala Ala Ala Met Ala Gly Asn Lys Ser Thr Pro Arg Ala Ser
     2690           1685           1690           1695
     2691 Ile Arg Pro Met Val Thr Pro Ala Thr Val Thr Asn Pro Thr Thr Thr
     2692           1700           1705           1710
     2693 Pro Thr Ala Thr Val Met Pro Thr Thr Gln Val Glu Ser Gln Glu Ala
     2694           1715           1720           1725
     2695 Met Gln Ser Glu Gly Pro Val Glu His Val Pro Val Phe Gly Ser Thr
     2696      1730           1735           1740
     2697 Ser Gly Ser Val Arg Ser Thr Ser Pro Asn Val Gln Pro Ser Ile Ser
E--> 2698 1745           1750           1755            ⊲1760
     2699 Gln Pro Ile Leu Thr Val Gln Gln Gln Thr Gln Ala Thr Ala Phe Val
     2700           1765           1770           1775
     2701 Gln Pro Thr Gln Gln Ser His Pro Gln Ile Glu Pro Ala Asn Gln Glu
     2702           1780           1785           1790
     2703 Leu Ser Ser Asn Ile Val Glu Val Val Gln Ser Ser Pro Val Glu Arg
     2704      1795           1800           1805
     2705 Pro Ser Thr Ser Thr Ala Val Phe Gly Thr Val Ser Ala Thr Pro Ser
     2706      1810           1815           1820
     2707 Ser Ser Leu Pro Lys Arg Thr Arg Glu Glu Glu Glu Asp Ser Thr Ile
E--> 2708 1825           1830           1835            ⊲1840
     2709 Glu Ala Ser Asp Gln Val Ser Asp Asp Thr Val Glu Met Pro Leu Pro
     2710           1845           1850           1855
     2711 Lys Lys Leu Lys Ser Val Thr Pro Val Gly Thr Glu Glu Glu Val Met
     2712           1860           1865           1870
     2713 Ala Glu Glu Ser Thr Asp Gly Glu Val Glu Thr Gln Val Tyr Asn Gln
     2714      1875           1880           1885
     2715 Asp Ser Gln Asp Ser Ile Gly Glu Gly Val Thr Gln Gly Asp Tyr Thr
     2716      1890           1895           1900
     2717 Pro Met Glu Asp Ser Glu Glu Thr Ser Gln Ser Leu Gln Ile Asp Leu
E--> 2718 1905           1910           1915            ⊲1920
     2719 Gly Pro Leu Gln Ser Asp Gln Gln Thr Thr Thr Ser Ser Gln Asp Gly
     2720           1925           1930           1935
     2721 Gln Gly Lys Gly Asp Asp Val Ile Val Ile Asp Ser Asp Asp Glu Glu
     2722           1940           1945           1950
     2723 Glu Asp Glu Glu Asp Asp Asp Asp Glu Asp Asp Thr Gly Met Gly
     2724      1955           1960           1965
     2725 Asp Glu Gly Glu Asp Ser Asn Glu Gly Thr Gly Ser Ala Asp Gly Asn
     2726      1970           1975           1980
```

RAW SEQUENCE LISTING   DATE: 12/26/2002
PATENT APPLICATION: US/09/762,577A   TIME: 13:32:08

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

```
      2727  Asp Gly Tyr Glu Ala Asp Asp Ala Glu Gly Gly Asp Gly Thr Asp Pro
E--> 2728  1985          1990          1995              2000
      2729  Gly Thr Glu Thr Glu Glu Ser Met Gly Gly Gly Glu Gly Asn His Arg
      2730                2005          2010              2015
      2731  Ala Ala Asp Ser Gln Asn Ser Gly Glu Gly Asn Thr Gly Ala Ala Glu
      2732                2020          2025              2030
      2733  Ser Ser Phe Ser Gln Glu Val Ser Arg Glu Gln Gln Pro Ser Ser Ala
      2734          2035          2040          2045
      2735  Ser Glu Arg Gln Ala Pro Arg Ala Pro Gln Ser Pro Arg Arg Pro Pro
      2736          2050          2055          2060
      2737  His Pro Leu Pro Pro Arg Leu Thr Ile His Ala Pro Pro Gln Glu Leu
E--> 2738  2065          2070          2075              2080
      2739  Gly Pro Pro Val Gln Arg Ile Gln Met Thr Arg Arg Gln Ser Val Gly
      2740                2085          2090              2095
      2741  Arg Gly Leu Gln Leu Thr Pro Gly Ile Gly Gly Met Gln Gln His Phe
      2742                2100          2105              2110
      2743  Phe Asp Asp Glu Asp Arg Thr Val Pro Ser Thr Pro Thr Leu Val Val
      2744          2115          2120          2125
      2745  Pro His Arg Thr Asp Gly Phe Ala Glu Ala Ile His Ser Pro Gln Val
      2746          2130          2135          2140
      2747  Ala Gly Val Pro Arg Phe Arg Phe Gly Pro Pro Glu Asp Met Pro Gln
E--> 2748  2145          2150          2155              2160
      2749  Thr Ser Ser Ser His Ser Asp Leu Gly Gln Leu Ala Ser Gln Gly Gly
      2750                2165          2170              2175
      2751  Leu Gly Met Tyr Glu Thr Pro Leu Phe Leu Ala His Glu Glu Glu Ser
      2752                2180          2185              2190
      2753  Gly Gly Arg Ser Val Pro Thr Thr Pro Leu Gln Val Ala Ala Pro Val
      2754          2195          2200          2205
      2755  Thr Val Phe Thr Glu Ser Thr Thr Ser Asp Ala Ser Glu His Ala Ser
      2756          2210          2215          2220
      2757  Gln Ser Val Pro Met Val Thr Thr Ser Thr Gly Thr Leu Ser Thr Thr
E--> 2758  2225          2230          2235              2240
      2759  Asn Glu Thr Ala Thr Gly Asp Asp Gly Asp Glu Val Phe Val Glu Ala
      2760                2245          2250              2255
      2761  Glu Ser Glu Gly Ile Ser Ser Glu Ala Gly Leu Glu Ile Asp Ser Gln
      2762                2260          2265              2270
      2763  Gln Glu Glu Glu Pro Val Gln Ala Ser Asp Glu Ser Asp Leu Pro Ser
      2764          2275          2280          2285
      2765  Thr Ser Gln Asp Pro Pro Ser Ser Ser Ser Val Asp Thr Ser Ser Ser
      2766          2290          2295          2300
      2767  Gln Pro Lys Pro Phe Arg Arg Val Arg Leu Gln Thr Thr Leu Arg Gln
E--> 2768  2305          2310          2315              2320
      2769  Gly Val Arg Gly Arg Gln Phe Asn Arg Gln Arg Gly Val Ser His Ala
      2770                2325          2330              2335
      2771  Met Gly Gly Arg Gly Gly Ile Asn Arg Gly Asn Ile Asn
      2772                2340          2345
      2777  02486/00109    215857.1
E--> 2780  1
```
—delete

VARIABLE LOCATION SUMMARY
PATENT APPLICATION: US/09/762,577A

DATE: 12/26/2002
TIME: 13:32:09

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

<u>Use of n's or Xaa's(NEW RULES):</u>
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:24; Xaa Pos. 2,4,7,16
Seq#:30; Xaa Pos. 9,14,15,20
Seq#:40; N Pos. 1,80,254,265,275,282,290,304
Seq#:42; N Pos. 15,22,24,76,77,119,153,163
Seq#:43; N Pos. 11,90,138,166,185,190,200
Seq#:49; N Pos. 163,168
Seq#:62; N Pos. 602
Seq#:63; N Pos. 35
Seq#:64; N Pos. 602
Seq#:65; N Pos. 17,25,37,41,53,68,70,144

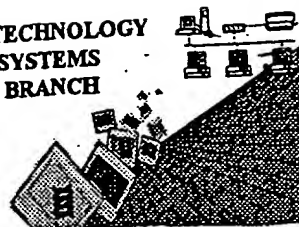VERIFICATION SUMMARY   DATE: 12/26/2002
PATENT APPLICATION: US/09/762,577A   TIME: 13:32:09

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF4\12262002\I762577A.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:630 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:1150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:16
L:1516 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:40
M:340 Repeated in SeqNo=40
L:1539 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:42
M:340 Repeated in SeqNo=42
L:1549 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:43
M:340 Repeated in SeqNo=43
L:1809 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1977 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:49
L:2278 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:2286 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:63
L:2310 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:2318 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:65
M:340 Repeated in SeqNo=65
L:2608 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:68
M:332 Repeated in SeqNo=68

0 S/1
Ψ B

RAW SEQUENCE LISTING
ERROR REPORT

A/I-8

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
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Date Processed by STIC: __12/26/02__

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

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Revised 01/29/2002